

Sub D1
SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Dawson, William O.
Grantham, George L.
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(ii) TITLE OF INVENTION: RECOMBINANT PLANT VIRAL
NUCLEIC ACIDS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent in Release #1.0,
Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 600,244
(B) FILING DATE: 22-OCT-1990

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 641,617
(B) FILING DATE: 16-JAN-1991

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 310,881
(B) FILING DATE: 17-FEB-1989

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 160,766
(B) FILING DATE: 26-FEB-1988

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 160,771
(B) FILING DATE: 26-FEB-1988

7,960X

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 347,637
(B) FILING DATE: 05-MAY-1989

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 363,138
(B) FILING DATE: 08-JUN-1989

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 219,279
(B) FILING DATE: 15-JUL-1988

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Halluin, Albert P.
(B) REGISTRATION NUMBER: 28,957
(C) REFERENCE/DOCKET NUMBER: B10G-20121 USA

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Pro Xaa Gly Pro
1

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGGTACCTGG GCC

13

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Chinese cucumber

(vii) IMMEDIATE SOURCE:

(B) CLONE: alpha-trichosanthin

(ix) FEATURE:

- (A) NAME/KEY: CDS (B) LOCATION: 8. .877
- (B) LOCATION: 8. .877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGAGG ATG ATC AGA TTC TTA GTC CTC TCT TTG CTA ATT CTC ACC CTG⁴⁹

Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu
1 5 10

TTC CTA ACA ACT CCT GCT GTG GAG GGC GAT GTT AGC TTC CGT TTA TCA⁹⁷

Phe Leu Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser
15 20 25 30

GGT GCA ACA AGC AGT TCC TAT GGA GTT TTC ATT TCA AAT CTG AGA AAA⁴⁵

Gly Ala Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys
35 40 45

GCT CTT CCA AAT GAA AGG AAA CTG TAC GAT ATC CCT CTG TTA CGT TCA⁹³

Ala Leu Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser

50

55

60

TCT CTT CCA GGT TCT CAA CGC TAC GCA TTG ATC CAT CTC ACA AAT ~~TAC~~ 41

Ser Leu Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr
65 70 75

GCC GAT GAA ACC ATT TCA GTG GCC ATA GAC ~~GTA~~ ACG AAC GTC TAT ~~AT~~ 29

Ala Asp Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile
80 85 90

ATG GGA TAT CGC GCT GGC GAT ACA TCC TAT TTT TTC AAC GAG GCT ~~TC~~ 37

Met Gly Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser
95 100 105 110

GCA ACA GAA GCT GCA AAA TAT GTA TTC AAA GAC GCT ATG CGA AAA ~~GT~~ 35

Ala Thr Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val
115 120 125

ACG CTT CCA TAT TCT GGC AAT TAC GAA AGG CTT CAA ACT GCT GCG ~~GC~~ 33

Thr Leu Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly
130 135 140

AAA ATA AGG GAA AAT ATT CCG CTT GGA CTC CCA GCT TTG GAC AGT ~~GC~~ 31

Lys Ile Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala
145 150 155

ATT ACC ACT TTG TTT TAC TAC AAC GCC AAT TCT GCT GCG TCG GCA ~~CT~~ 29

Ile Thr Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu
160 165 170

ATG GTA CTC ATT CAG TCG ACG TCT GAG GCT GCG AGG TAT AAA TTT ~~AT~~ 7

Met Val Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile
175 180 185 190

GAG CAA CAA ATT GGG AAG CGC GTT GAC AAA ACC TTC CTA CCA AGT ~~TT~~ 25

Glu Gln Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu
195 200 205

GCA ATT ATA ACT TTG GAA AAT AGT TGG TCT GCT CTC TCC AAG CAA ~~AT~~ 73

Ala Ile Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile
210 215 220

CAG ATA GCG AGT ACT AAT AAT GGA CAG TTT GAA ACT CCT GTT GTG CTC²¹
Gln Ile Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu
225 230 235

ATA AAT GCT CAA AAC CAA CGA GTC ATG ATA ACC AAT GTT GAT GCT GGA⁶⁹
Ile Asn Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly
240 245 250

GTT GTA ACC TCC AAC ATC GCG TTG CTG CTG NAT CGA AAC AAT ATG GCA¹⁷
Val Val Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala
255 260 265 270

GCC ATG GAT GAC GAT GTT CCT ATG ACA CAG AGC TTT GGA TGT GGA AGC⁶⁵
Ala Met Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser
275 280 285

TAT GCT ATT TAGTAACTCG AG 886

Tyr Ala Ile 290

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1 Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu Phe Leu
1 5 10 15

Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser Gly Ala
20 25 30

Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys Ala Leu
35 40 45

Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser Ser Leu
50 55 60

Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr Ala Asp
65 70 75 80

100

Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile Met Gly
85 90 95

Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser Ala Thr
100 105 110

Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val Thr Leu
115 120 125

Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly Lys Ile
130 135 140

Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala Ile Thr
145 150 155 160

Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu Met Val
165 170 175

Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile Glu Gln
180 185 190

Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu Ala Ile
195 200 205

Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile Gln Ile
210 215 220

Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu Ile Asn
225 230 235 240

Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly Val Val
245 250 255

Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala Ala Met
260 265 270

Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser Tyr Ala
275 280 285

Ile

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

101

(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa
(vii) IMMEDIATE SOURCE:
(B) CLONE: alpha-amylase
(ix) FEATURE:
(A) NAME/KEY: CDS (B) LOCATION: 12. .1316
(B) LOCATION: 12. .1316
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCTCGAGGTG C ATG CAG GTG CTG AAC ACC ATG GTG AAC A CAC TTC TTG 50

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu
1 5 10

TCC CTT TCG GTC CTC ATC GTC CTC CTT GGC CTC TCC TCC AAC TTG AC~~A~~98

Ser Leu Ser Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr
15 20 25

GCC GGG CAA GTC CTG TTT CAG GGA TTC AAC TGG GAG TCG TGG AAG GA~~A~~46

Ala Gly Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu
30 35 40 45

AAT GGC GGG TGG TAC AAC TTC CTG ATG GGC AAG GTG GAC GAC ATC GA~~A~~94

Asn Gly Gly Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala
50 55 60

GCA GCC GGC ATC ACC CAC GTC TGG CTC CCT CCG CCG TCT CAC TCT G~~T~~242

Ala Ala Gly Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val
65 70 75

GGC GAG CAA GGC TAC ATG CCT GGG CGG CTG TAC GAT CTG GAC GCG TC~~T~~90

Gly Glu Gln Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser
80 85 90

AAG TAC GGC AAC GAG GCG CAG CTC AAG TCG CTG ATC GAG GCG TTC CA~~A~~8

Lys Tyr Gly Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His
95 100 105

GGC AAG GGC GTC CAG GTG ATC GCC GAC ATC GTC ATC AAC CAC CGC ~~ACB6~~
Gly Lys Gly Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr
110 115 120 125

GCG GAG CAC AAG GAC GGC CGC GGC ATC TAC TGC CTC TTC GAG GGC ~~CGA84~~
Ala Glu His Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly
130 135 140

ACG CCC GAC TCC CGC CTC GAC TGG GGC CCG CAC ATG ATC TGC CGC ~~GA82~~
Thr Pro Asp Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp
145 150 155

GAC CCC TAC GGC CAT GGC ACC GGC AAC CCG GAC ACC GGC GCC GAC ~~TG80~~
Asp Pro Tyr Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe
160 165 170

GCC GCC GCG CCG GAC ATC GAC CAC CTC AAC AAG CGC GTC CAG CGG ~~GA88~~
Ala Ala Ala Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu
175 180 185

CTC ATT GGC TGG CTC GAC TGG CTC AAG ATG GAC ATC GGC TTC GAC ~~GA826~~
Leu Ile Gly Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala
190 195 200 205

TGG CGC CTC GAC TTC GGC AAG GGC TAC TCC GCC GAC ATG GCA AAC ~~AK84~~
Trp Arg Leu Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile
210 215 220

TAC ATC GAC GCC ACC GAG CCG AGC TTC GCC GTG CCC GAG ATA TCG ~~AC822~~
Tyr Ile Asp Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr
225 230 235

TCC ATG GCG AAC GGC GGG GAC GGC AAG CCG AAC TAC GAC CAG AAC ~~CG80~~
Ser Met Ala Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala
240 245 250

CAC CGG CAG GAG CTG GTC AAC TGG GTC GAT CGT GTC GGC GGC GCC ~~AC818~~
His Arg Gln Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn
255 260 265

ACC AAC GGC ACG GCG TTC GAC TTC ACC ACC AAG GGC ATC CTC AAC ~~GE866~~

Ser Asn Gly Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val
270 275 280 285

GCC GTG GAG GGC GAG CTG TGG CGC CTC CGG GGC GAG GAC GGC AAG GGG~~14~~

Ala Val Glu Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala
290 295 300

CCC GGC ATG ATC GGG TGC TGG CCG GCC AAG GCG ACG ACC TTC GTC GAA~~52~~

Pro Gly Met Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp
305 310 315

AAC CAC GAC ACC GGC TCG ACC CAG CAC CTG TGG CCG TTC CCC TCC GAA~~10~~

Asn His Asp Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp
320 325 330

AAG GTC ATG CAG GGC TAC GCA TAC ATC CTC ACC CAC CCC GGC AAC GAA~~58~~

Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro
335 340 345

TGC ATC TTG TAC GAC CAT TTC TTC GAT TGG GGT CTC AAG GAG GAG AAG~~96~~

Cys Ile Phe Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile
350 355 360 365

GAG CGC CTG GTG TCA ATC AGA AAC CGG CAG GGG ATC CAC CCG GCG AGG~~54~~

Glu Arg Leu Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser
370 375 380

GAG CTG CGC ATG ATG GAA GCT GAC AGC GAT CTC TAC CTC GCG GAG AAG~~2~~

Glu Leu Arg Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile
385 390 395

GAT GGC AAG GTG ATC ACA AAG ATT GGA CCA AGA TAC GAC GTC GAA GAG~~50~~

Asp Gly Lys Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His
400 405 410

CTC ATC CCC GAA GGC TTC CAG GTC GCG CAC GGT GAT GGC TAC GCA~~98~~

Leu Ile Pro Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala
415 420 425

ATC TGG GAG AAA ATC TGAGCGCACG ATGACGAGAC TCTCAGTTA GCAGATT~~53~~

Ile Trp Glu Lys Lle
430 435

CCTGCGATTT TTACCCCTGAC CGGTATACTGT ATATACGTGC CGGCAACGAG
CTGTATCCGA

1413

TCCGAATTAC GGATGCAATT GTCCACGAAG TCCTCGAGG

1452

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 amino acids
(B) TYPE: amino acid
(D) Topology: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1 5 10 15

Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Gln
20 25 30

Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu Asn Gly Gly
35 40 45

Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala Ala Gly
50 55 60

Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val Gly Glu Gln
65 70 75 80

Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly
85 90 95

Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His Gly Lys Gly
100 105 110

Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr Ala Glu His
115 120 125

Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly Thr Pro Asp
130 135 140

Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp Asp Pro Tyr
145 150 155 160

Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe Ala Ala Ala
165 170 175

105

Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu Leu Ile Gly
180 185 190

Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala Trp Arg Leu
195 200 205

Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile Tyr Ile Asp
210 215 220

Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr Ser Met Ala
225 230 235 240

Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala His Arg Gln
245 250 255

Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn Ser Asn Gly
260 265 270

Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val Ala Val Glu
275 280 285

Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala Pro Gly Met
290 295 300

Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp Asn His Asp
305 310 315 320

Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp Lys Val Met
325 330 335

Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro Cys Ile Phe
340 345 350

Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile Glu Arg Leu
355 360 365

Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser Glu Leu Arg
370 375 380

Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile Asp Gly Lys
385 390 395 400

Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His Leu Ile Pro
405 410 415

Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala Ile Trp Glu
420 425 430

Lys Ile

166

(2)

INFORMATION FOR SEQ ID NO:7:

(i)

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (G) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii)

MOLECULE TYPE: cDNA to mRNA

(iii)

HYPOTHETICAL: NO

(iv)

ANTI-SENSE: NO

(vi)

ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii)

IMMEDIATE SOURCE:

- (B) CLONE: alpha-hemoglobin

(ix)

FEATURE:

- (A) NAME/KEY: transit_peptide (B) LOCATION:
26. .241
- (B) LOCATION: 26. .241

(ix)

FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 245. .670

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGAGGGCA TCTGATCTTT CAAGAATGGC ACAAAATTAAC AACATGGCAC
AAGGGATACA

60

AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT
CAAGTTTCTT

120

TGTTTTGGA TGAAAAAAC TGAAAATTC AGCAAATTCT ATGTTGGTT TGAAAAAAAG

TTCAATTTTT ATGCAAAAGT TTTGTTCCCTT TAGGATTTCAGCAGGTGGTA
GACTTTCTG

240

CATG GTG CTG TCT CCT GCC GAC AAG ACC AAC GTC AAG GCC GCC TGG GGC
289

Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Clys
1 5 10 15

AAG GTT GGC GCG CAC GCT GGC GAG TAT GGT GCG GAG GCC CTG GAG AGG

Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg
20 25 30

107

ATG TTC CTG TCC TTC CCC ACC ACC AAG ACC TAC TTC CCG CAC TTC G**A**85
Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp
35 40 45

CTG AGC CAC GGC TCT GCC CAG GTT AAG GGC CAC GGC AAG AAG GTG G**G**33
Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala
50 55 60

GAC GCG CTG ACC AAC GCC GTG GCG CAC GTG GAC GAC ATG CCC AAC G**G**81
Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala
65 70 75

CTG TCC GCC CTG AGC GAC CTG CAC GCG CAC AAG CTT CGG GTG GAC G**G**29
Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro
80 85 90 95

GTC AAC TTC AAG CTC CTA AGC CAC TGC CTG CTG GTG ACC CTG GCC G**G**77
Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala
100 105 110

CAC CTC CCC GCC GAG TTC ACC CCT GCG GTG CAC GCC TCC CTG GAC A**A**25
His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys
115 120 125

TTC CTG GCT TCT GTG AGC ACC GTG CTG ACC TCC AAA TAC CGT
TAAGCTGGAG 677

Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
130 135 140

CCTCGGTAGC CGTTCCCTCCT GCCCGGTCGA CC

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:8:

108

Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys
1 5 10 15

Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
20 25 30

Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
35 40 45

Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
50 55 60

Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
65 70 75 80

Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
85 90 95

Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
100 105 110

Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
115 120 125

Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: beta-hemoglobin

(ix) FEATURE:

(A) NAME/KEY: transit_peptide (B) LOCATION:
26. .241

109

(B) LOCATION: 26..241

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 245..685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTCGAGGGGA TCTGATCTT CAAGAATGGC ACAAAATTAAC AACATGGCAC
AAGGGATACA

60

AACCCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT
CAAGTTTCTT

120

TGTTTTGGA TCTAAAAAAC TGAAAAATTC AGCAAATTCT ATGTTGGTTT
TGAAAAAAAGA

180

TTCAATTTT ATGCAAAAGT TTTGTTCTT TAGGATTCA GCAGGTGGTA
GAGTTTCTT

240

GATG GTG CAC CTG ACT CCT GAG GAG AAG TCT GCC GTT ACT GCC CTG TGG
289

Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp
1 5 10 15

GGC AAG GTG AAC GTG GAT GAA GTT GGT GGT GAG GCC CTG GGC AGG CTG 37

Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
20 25 30

CTG GTG GTC TAC CCT TGG ACC CAG AGG TTC TTT GAG TCC TTT GGG GAT 35

Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp
35 40 45

CTG TCC ACT CCT GAT GCT GTT ATG GGC AAC CCT AAG GTG AAG GCT CAG 33

Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His
50 55 60

GGC AAG AAA GTG CTG GGT GGC TTT AGT GAT GGC CTG GCT CAC CTG GAG 31

Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp
65 70 75

AAC CTC AAG GGC ACC TTT GCC ACCA CTG AGT GAG CTG CAC TGT GAC AAG
529

Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
80 85 90 95

116

-109-

CTG CAC GTG GAT CCT GAG AGC TTC AGG CTC CTA GGC AAC GTG CTG G**CG**7

Leu His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val
100 105 110

TGT GTG CTG GCG CAT CAC TTT GGC AAA GAA TTC ACC CCA CCA GTG C**AG**25

Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln
115 120 125

GCT GCC TAT CAG AAA GTG GTG GCT GGT GTG GCT AAT GCC CTG GCC C**AG**3

Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His
130 135 140

AAG TAT CAC TAAGCTCGCT TTCTTGCTGT CCAATTCTA TTAAAGGTTTC 722

Lys Tyr His
145

CTTTGTGGGG TCGAGGTCGA C 743

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly
1 5 10 15

Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
20 25 30

Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
35 40 45

Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
50 55 60

Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn
65 70 75 80

Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu
85 90 95

-110-

His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val Cys
100 105 110

Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
115 120 125

Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
130 135 140

Tyr His
145

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: alkalophilic Bacillus sp.
- (B) STRAIN: 38-2

(vii) IMMEDIATE SOURCE:

- (B) CLONE: beta-cyclodextrin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala Pro Asp Thr Ser Val Ser Asn Lys Gln Asn Phe Ser Thr Asp Val
1 5 10 15

Ile

112